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<170>   PatentIn version 3.1

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Ala Gly Gln Gln Trp Ala Leu Gln Thr Val Leu Leu Glu Val Leu Asn
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Ile Pro Leu Lys Phe Pro Asp Pro Val Asn Thr Gly Ser Lys Arg Pro
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Thr Tyr Tyr Glu Ser Phe Pro Ser Ser Gly Gly Glu Gly Ala Ile Pro
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Val Leu Asp Tyr Asn Pro Asp Asn Ser Pro Thr Ala Pro Leu Tyr Leu
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Arg Phe Gly Pro Asp Arg Phe Phe Glu Ile Leu Ile Pro Ser Pro Thr
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Lys Glu Arg Val His Phe Phe Ala Glu Thr Gly Ile Thr Phe Arg Pro
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Asp Val Phe Lys Thr Arg Ser Val Val Pro Ala Glu Glu Pro Val Glu
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Gln Arg Thr Glu Phe Lys Val Ser Gln Met Leu Asp Trp Leu Leu Gln
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Gln Leu Gly Leu Ser Lys Thr Tyr Ala Ile Met Thr Leu Glu Pro His
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Gln Ile Arg His His Lys Thr Asp Leu Leu Ser Pro Ser Gly Thr Gly
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Glu Val Met Asn Asp Gly Val Gly Arg Met Ser Arg Ser Val Ala Lys
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Arg Ile Arg Asp Val Leu Gly Leu Gly Asp Val Pro Ser Ala Val Gln
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Gly Arg Phe Gly Ser Ala Lys Gly Met Trp Val Ile Asp Val Asp Asp
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    Val Phe Lys Pro Glu Leu His Ser Leu Lys Asp Val Ile Ile Phe Ser
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Met Cys  Thr Asn Tyr Lys Glu  Arg Leu Cys Tyr Ile  Asn Asn Ser
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Val Ser  Asn Lys Pro Ala Ile  Ile Leu Ser Ser Leu  Val Gly Asn
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Leu Val  Asp Gln Ser Lys Gln  Gly Ile Val Phe Asn  Glu Ala Ser
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Arg Pro Gly Glu Gly Ala Pro Ala Leu Met Thr Ala Phe Met Tyr
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Ala Gly Leu Met Pro Asp Lys Lys Phe Thr Lys Gln Tyr Val Ala
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Arg Leu Glu Gly Asp Gly Ser Glu Tyr Pro Asp Pro Glu Val Tyr
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Met His Cys Lys Val Asp Leu Glu Asp Glu Ser Leu Gly Leu Lys Tyr
    50                  55                  60


Asp Pro Ser Trp Ser Thr Ala Arg Asp Val Thr Asp Ile Trp Lys Thr
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Leu Tyr Arg Leu Asp Ala Phe Arg Gly Lys Pro Phe Pro Glu Lys Pro
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Glu Gln Gly Cys Arg Leu Thr Arg Arg Phe Gly Pro Asp Arg Phe Phe
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Glu Ile Leu Ile Pro Ser Pro Thr Ser Thr Ser Pro Ser Val Pro Pro
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Val Val Ser Lys Gln Pro Gly Ala Val Glu Glu Val Ile Gln Trp Leu
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Thr Met Gly Gln His Ser Leu Val Gly Arg Gln Trp Arg Ala Phe Phe
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Val Pro Ala Glu Glu Pro Val Glu Gln Arg Thr Glu Phe Lys Val Ser
            260             265             270

Gln Met Leu Asp Trp Leu Leu Gln Leu Asp Asn Asn Thr Trp Gln Pro
            275             280             285

His Leu Lys Leu Phe Ser Arg Ile Gln Leu Gly Leu Ser Lys Thr Tyr
            290             295             300

Ala Ile Met Thr Leu Glu Pro His Gln Ile Arg His His Lys Thr Asp
305             310             315             320

Leu Leu Ser Pro Ser Gly Thr Gly Glu Val Met Asn Asp Gly Val Gly
                325             330             335

Arg Met Ser Arg Ser Val Ala Lys Arg Ile Arg Asp Val Leu Gly Leu
```

                    340   345   350

        Gly Asp Val Pro Ser Ala Val Gln Gly Arg Phe Gly Ser Ala Lys Gly
                355   360   365

        Met Trp Val Ile Asp Val Asp Asp Thr Gly Asp Glu Asp Trp Ile Glu
                370   375   380

        Thr Tyr Pro Ser Gln Arg Lys Trp Glu Cys Asp Phe Val Asp Lys His
        385   390   395   400

        Gln Arg Thr Leu Glu Val Arg Ser Val Ala Ser Glu Leu Lys Ser Ala
                            405   410   415

        Gly Leu Asn Leu Gln Leu Leu Pro Val Leu Glu Asp Arg Ala Arg Asp
                        420   425   430

        Lys Val Lys Met Arg Gln Ala Ile Gly Asp Arg Leu Ile Asn Asp Leu
                435   440   445

        Gln Arg Gln Phe Ser Glu Gln Lys His Ala Leu Asn Arg Pro Val Glu
                450   455   460

        Phe Arg Gln Trp Val Tyr Glu Ser Tyr Ser Ser Arg Ala Thr Arg Val
        465   470   475   480

        Ser His Gly Arg Val Pro Phe Leu Ala Gly Leu Pro Asp Ser Gln Glu
                        485   490   495

        Glu Thr Leu Asn Phe Leu Met Asn Ser Gly Phe Asp Pro Lys Lys Gln
                    500   505   510

        Lys Tyr Leu Gln Asp Ile Ala Trp Asp Leu Gln Lys Arg Lys Cys Asp
                    515   520   525

        Thr Leu Lys Ser Lys Leu Asn Ile Arg Val Gly Arg Ser Ala Tyr Ile
                530   535   540

        Tyr Met Ile Ala Asp Phe Trp Gly Val Leu Glu Glu Asn Glu Val His
        545   550   555   560

        Val Gly Phe Ser Ser Lys Phe Arg Asp Glu Glu Glu Ser Phe Thr Leu
                        565   570   575

        Leu Ser Asp Cys Asp Val Leu Val Ala Arg Ser Pro Ala His Phe Pro
                    580   585   590

```
Ser Asp Ile Gln Arg Val Arg Ala Val Phe Lys Pro Glu Leu His Ser
    595             600             605

Leu Lys Asp Val Ile Ile Phe Ser Thr Lys Gly Asp Val Pro Leu Ala
    610             615             620

Lys Lys Leu Ser Gly Gly Asp Tyr Asp Gly Asp Met Ala Trp Val Cys
625             630             635             640

Trp Asp Pro Glu Ile Val Asp Gly Phe Val Asn Ala Glu Met Pro Leu
            645             650             655

Glu Pro Asp Leu Ser Arg Tyr Leu Lys Lys Asp Lys Thr Thr Phe Lys
            660             665             670

Gln Leu Met Ala Ser His Gly Thr Gly Ser Ala Ala Lys Glu Gln Thr
    675             680             685

Thr Tyr Asp Met Ile Gln Lys Ser Phe His Phe Ala Leu Gln Pro Asn
    690             695             700

Phe Leu Gly Met Cys Thr Asn Tyr Lys Glu Arg Leu Cys Tyr Ile Asn
705             710             715             720

Asn Ser Val Ser Asn Lys Pro Ala Ile Ile Leu Ser Ser Leu Val Gly
            725             730             735

Asn Leu Val Asp Gln Ser Lys Gln Gly Ile Val Phe Asn Glu Ala Ser
            740             745             750

Trp Ala Gln Leu Arg Arg Glu Leu Leu Gly Gly Ala Leu Ser Leu Pro
    755             760             765

Asp Pro Met Tyr Lys Ser Asp Ser Trp Leu Gly Arg Gly Glu Pro Thr
    770             775             780

His Ile Ile Asp Tyr Leu Lys Phe Ser Ile Ala Arg Pro Ala Ile Asp
785             790             795             800

Lys Glu Leu Glu Ala Phe His Asn Ala Met Lys Ala Ala Lys Asp Thr
            805             810             815

Glu Asp Gly Ala His Phe Trp Asp Pro Asp Leu Ala Ser Tyr Tyr Thr
            820             825             830
```

```
Phe Phe Lys Glu Ile Ser Asp Lys Ser Arg Ser Ser Ala Leu Leu Phe
        835             840             845


Thr Thr Leu Lys Asn Arg Ile Gly Glu Val Glu Lys Glu Tyr Gly Arg
    850             855             860


Leu Val Lys Asn Lys Glu Met Arg Asp Ser Lys Asp Pro Tyr Pro Val
865             870             875             880


Arg Val Asn Gln Val Tyr Glu Lys Trp Cys Ala Ile Thr Pro Glu Ala
            885             890             895


Met Asp Lys Ser Gly Ala Asn Tyr Asp Ser Lys Val Ile Arg Leu Leu
        900             905             910


Glu Leu Ser Phe Leu Ala Asp Arg Glu Met Asn Thr Trp Ala Leu Leu
        915             920             925


Arg Ala Ser Thr Ala Phe Lys Leu Tyr Tyr His Lys Ser Pro Lys Phe
    930             935             940


Val Trp Gln Met Ala Gly Arg Gln Leu Ala Tyr Ile Lys Ala Gln Met
945             950             955             960


Thr Ser Arg Pro Gly Glu Gly Ala Pro Ala Leu Met Thr Ala Phe Met
            965             970             975


Tyr Ala Gly Leu Met Pro Asp Lys Lys Phe Thr Lys Gln Tyr Val Ala
        980             985             990


Arg Leu Glu Gly Asp Gly Ser Glu  Tyr Pro Asp Pro Glu  Val Tyr Glu
    995             1000            1005


Val Leu  Gly Asp Asp Asp Phe  Asp Gly Ile Gly Phe  Thr Gly Asn
    1010            1015            1020


Gly Asp  Tyr
    1025


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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial sequence is primer
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<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial sequence is primer

<400>  6
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<210>  7
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial sequence is primer

<400>  7
gccaagcttc catgaaccct attactccta                              30


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<211>  28
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial sequence is primer

<400>  8
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<210>  9
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial sequence is primer

<400>  9
gctcaaatcc catggctcgg agcgaagaaa                              30


<210>  10
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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  artificial sequence is primer

<400>  10
```

```
ccgaattcta ataatcgcca ttccctgtga                               30
```

```
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<211>   20
<212>   RNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   11
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```

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<210>   12
<211>   20
<212>   RNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   12
cgacucaugg accuugggag                                          20
```

```
<210>   13
<211>   8
<212>   PRT
<213>   Neurospora crassa

<220>
<221>   MISC_FEATURE
<222>   (1)..(8)
<223>   Xaa is any amino acid


<400>   13

Gly Ser Asp Leu Asp Gly Asp Xaa
1               5
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```
<210>   14
<211>   129
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is tag sequence

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gaattctgca gatatccagc acagtggcgg ccgctcgagt ctagagggcc cttcgaaggt    60

aagcctatcc ctaaccctct cctcggtctc gattctacgc gtaccggtca tcatcaccat   120

caccattga                                                           129
```

```
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```

```
<211>  42
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<213>  Artificial Sequence

<220>
<223>  artificial sequence is tag sequence

<400>  15

Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu Ser Arg Gly
1               5                   10                  15


Pro Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
            20                  25                  30


Thr Arg Thr Gly His His His His His His
            35                  40
```